

QY 256 ATSSSFTTNSHVSQNRHGRGQPCSPORCOPPCASCPHENILPKYKTSWRPPPKRSD 315  
DB 241 ATSSSFTTNSHVSQNRHGRGQPCSPORCOPPCASCPHENILPKYKTSWRPPPKRSD 300  
QY 316 RKDVQHNWYIGEYSRQAEVEAFMKNKDGSLVDRDCSTKSKBEPVLAFFVFNKYNVVK 375  
DB 301 RKDVQHNWYIGEYSRQAEVEAFMKNKDGSLVDRDCSTKSKBEPVLAFFVFNKYNVVK 360  
QY 376 IRFLERNQOPALGTGLRGDEKDSVEDIIEHYKNPPIILIDGKDTGVHRKQCHLTQPLP 435  
DB 361 IRFLERNQOPALGTGLRGDEKDSVEDIIEHYKNPPIILIDGKDTGVHRKQCHLTQPLP 420  
QY 436 LTRHLLPL 443  
DB 421 LTRHLLPL 428

## SEQUENCE COMPARISON 'A'

RESULT 2  
Q9P2U9 HUMAN PRELIMINARY; PRT; 376 AA.  
AC Q9P2U9; integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2000, sequence version 1.  
DT 07-FEB-2006, entry version 15.  
DE MIST (Fragment).  
GN Name=MIST;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RX [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=20208989; PubMed=10744659; DOI=10.1093/intimm/12.4.573;  
RA Goitsuka R., Kanazashi H., Sasunuma H., Fujimura Y., Hidaka Y.,  
RA Tatsuno A., Ra C., Hayashi K., Kitamura D.;  
RT "A BASH/SIP-76-related adaptor protein MIST/Clnk involved in Ige  
RT receptor-mediated mast cell degranulation."  
RL Int. Immunol. 12:573-580(2000).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB032369; BAA96241.1; -; mRNA.  
DR HSSP; Q06124; 2SHP.  
DR Ensembl; ENSG00000109684; Homo sapiens.  
DR GO; GO:0005622; C:intracellular; NAS.  
DR GO; GO:0005070; F:SH3/SH2 adaptor activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR GO; GO:0007242; P:intracellular signaling cascade; IDA.  
DR InterPro; IPR000980; SH2.  
DR Pfam; PF00017; SH2; 1.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR ProDom; PD000093; SH2; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; PS50001; SH2; 1.  
FT NON\_TER 376 376  
FT TER 1 1  
SQ SEQUENCE 376 AA; 43542 MW; 389421B629B028B2 CRC64;

Query Match 84.7%; Score 2009; DB 2; Length 376;  
Best Local Similarity 99.5%; Pred. No. 6.9e-120;  
Matches 374; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 34 FQNSLPKNSWRPINSATGQYQRMNKPFLDWRNFAAALDCAKSHSDDDYDDPELRNEE 93  
DB 1 FQNSLPKNSWRPINSATGQYQRMNKPFLDWRNFAAALDCAKSHSDDDYDDPELRNEE 60  
QY 94 TQSIKILPARIKESEYADTHYFKVAMDTPLDTRTSISIGQPTWNTQRLERVDKPI 153  
DB 61 TQSIKILPARIKESEYADTHYFKVAMDTPLDTRTSISIGQPTWNTQRLERVDKPI 120  
QY 154 SKDVSQNIKGASVRKNKIPLPPLRPLTLPKYQPLPPESPSPPLSRHTFPFVQR 213

DB 121 SRDVSQNIKGASVRKNKIPLPPLRPLTLPKYQPLPPESPSPPLSRHTFPFVQR 180  
QY 214 MPSQISRLDLSEVLEAKVPHNQKPSSTHLENQNTQEIPLAISSSSFTTNSHVSQNRD 273  
DB 181 MPSQISRLDLSEVLEAKVPHNQKPSSTHLENQNTQEIPLAISSSSFTTNSHVSQNRD 240  
QY 274 HRGQPCSPORCOPPCASCPHENILPKYKTSWRPPPKRSDRKDVQHNWYIGEYSRQA 333  
DB 241 HRGQPCSPORCOPPCASCPHENILPKYKTSWRPPPKRSDRKDVQHNWYIGEYSRQA 300  
QY 334 VERAFMKNKDGSLVDRDCSTKSKBEPVLAFFVFNKYNVVKIRFLERNQOPALGTGLRG 393  
DB 301 VERAFMKNKDGSLVDRDCSTKSKBEPVLAFFVFNKYNVVKIRFLERNQOPALGTGLRG 360  
QY 394 DEKFDSDVEDIIEHYKN 409  
DB 361 DEKFDSDVEDIIEHYKN 376

RESULT 3  
Q9JMJ3 MOUSE PRELIMINARY; PRT; 435 AA.  
AC Q9JMJ3; integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2000, sequence version 1.  
DT 07-FEB-2006, entry version 19.  
DE MIST.  
GN Name=Clnk; Synonyms=MIST;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RX [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=20208989; PubMed=10744659; DOI=10.1093/intimm/12.4.573;  
RA Goitsuka R., Kanazashi H., Sasunuma H., Fujimura Y., Hidaka Y.,  
RA Tatsuno A., Ra C., Hayashi K., Kitamura D.;  
RT "A BASH/SIP-76-related adaptor protein MIST/Clnk involved in Ige  
RT receptor-mediated mast cell degranulation."  
RL Int. Immunol. 12:573-580(2000).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB021220; BAA96240.1; -; mRNA.  
DR HSSP; P00524; INZL.  
DR Ensembl; ENSMUSG00000039315; Mus musculus.  
DR MGI; MGI:1351468; Clnk.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0007242; P:intracellular signaling cascade; RCA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IDA.  
DR InterPro; IPR000980; SH2.  
DR Pfam; PF00017; SH2; 1.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR ProDom; PD000093; SH2; 1.  
DR SMART; SM00252; SH2; 1.  
DR PROSITE; PS50001; SH2; 1.  
SQ SEQUENCE 435 AA; 49513 MW; 4D1BD3E32F0C61ED6 CRC64;

Query Match 55.5%; Score 1316.5; DB 2; Length 435;  
Best Local Similarity 62.1%; Pred. No. 1.1e-75;  
Matches 266; Conservative 46; Mismatches 111; Indels 5; Gaps 4;  
QY 16 MNRQGNKTKESNDLKFQNSLPKNSWRPINSATGQYQRMNKPFLDWRNFAAALDVG 75  
DB 1 MTSQGNKTKESFGDURFQNSLLKNSWFLSSAKRCEAVLEPLDHRNLAVPGG 60  
QY 76 AKGSHDDDDYDDPELRNEEETWQSIKILPARIKESEYADTHYFKVAMDTPLDTRTSISI 135  
DB 61 EKCNSNDYDDPELRNEEETWQSIKILPARIKESEYADTHYFKVAMDTPLDTRTSISI 120